CRF Errors Corrected by th STIC Systems Branch

Serial Number: 08/819,669 E

ENTERED **RECEIVED**

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☑ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: 8, 24
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____.
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☑ Other: _Seq 17, 27 - replaced; w/colon_

*Examiner: The above corrections must be communicated to the applicant in th first Office Action. DO NOT send a copy of this form.

3/1/95

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

```
 1                                    SEQUENCE LISTING
 2
 3    (1)     General Information:
 4
 5          (i)   APPLICANTS:  Boon-Falleur, Thierry; Van der Bruggen, Thierry;
 6                Van den Eynde, Beno t; Van Pel, Aline; De Plaen, Etienne;
 7                Lurquin, Christophe; Chomez, Patrick; Traversari, Catia
 8
 9          (ii) TITLE OF INVENTION:  Tumor Rejection Antigen Precursors, Tumor
10                Rejection Antigens and Uses Thereof
11
12          (iii) NUMBER OF SEQUENCES:  28
13
14          (iv) CORRESPONDENCE ADDRESS:
15                (A) ADDRESSEE: Fulbright & Jaworski LLP
16                (B) STREET: 666 Fifth Avenue
17                (C) CITY:  New York City
18                (D) STATE:  New York
19                (E) COUNTRY; USA
20                (F) ZIP:  10103
21
22          (v) COMPUTER READABLE FORM:
23                (A) MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
24                (B) COMPUTER:  IBM
25                (C) OPERATING SYSTEM:  PC-DOS
26                (D) SOFTWARE:  Wordperfect
27
28          (vi) CURRENT APPLICATION DATA:
29                (A) APPLICATION NUMBER:  08/819,669
30                (B) FILING DATE: 17-March-1997
31                (C) CLASSIFICATION:  435
32
33          (vii) PRIOR APPLIATION DATA:
34                (A) APPLICATION NUMBER: 08/142,368
35                (B) FILING DATE: 02-MAY-1994
36
37          (vii) PRIOR APPLICATION DATA:
38                (A) APPLICATION NUMBER:  PCT/US92/04354
39                (B) FILING DATE:  22-MAY-1992
40
41          (vii) PRIOR APPLICATION DATA:
42                (A) APPLICATION NUMBER:  07/807,043
43                (B) FILING DATE:  12-DECEMBER-1991
44
45          (vii) PRIOR APPLICATION DATA:
46                (A) APPLICATION NUMBER:  07/764,364
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47              (B) FILING DATE:   23-SEPTEMBER-1991
48
49        (vii) PRIOR APPLICATION DATA:
50              (A) APPLICATION NUMBER: 07/728,838
51              (b) FILING DATE:  9-JULY-1991
52
53        (vii) PRIOR APPLICATION DATA:
54              (A) APPLICATION NUMBER:  07/705,702
55              (B) FILING DATE:  23-May-1991
56
57        (viii) ATTORNEY/AGENT INFORMATION:
58              (A) NAME:  Hanson, Norman D.
59              (B) REGISTRATION NUMBER:  30,946
60              (C) REFERENCE/DOCKET NUMBER:  LUD 5253.5-US
61
62        (ix) TELECOMMUNICATION INFORMATION:
63              (A) TELEPHONE: (212)318-3168
64              (B) TELEFAX: (212)752-5958
65
66
67
68   (2) INFORMATION FOR SEQ ID NO: 1:
69        (i) SEQUENCE CHARACTERISTICS:
70              (A) LENGTH:   462 base pairs
71              (B) TYPE:  nucleic acid
72              (C) STRANDEDNESS: single
73              (D) TOPOLOGY:   linear
74        (ii) MOLECULE TYPE:  genomic DNA
75        (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 1:
76
77
78
79
80   ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT GAAGATCCTG        60
81   ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT CAGCCAATGA GCTTACTGTT       120
82   CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG       180
83   CTTGTGAATT TGTACCCTTT CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC       240
84   CCCCCTCCCA CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT       300
85   AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCCTTT GCTCTCCCAG CATGCATTGT       360
86   GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG CTAGCTTGCG ACTCTACTCT       420
87   TATCTTAACT TAGCTCGGCT TCCTGCTGGT ACCCTTTGTG CC                        462
88
89
90
91   (2) INFORMATION FOR SEQ ID NO: 2:
92        (i) SEQUENCE CHARACTERISTICS:
93              (A) LENGTH:   675 base pairs
94              (B) TYPE:  nucleic acid
95              (C) STRANDEDNESS: single
96              (D) TOPOLOGY:   linear
97        (ii) MOLECULE TYPE:  genomic DNA
98        (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 2:
99
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100
101    ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA GGT GGT        48
102    Met Ser Asp Asn Lys Lys Pro Asp Lys Ala His Ser Gly Ser Gly Gly
103                     5                      10                      15
104    GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG TAC TCC CTG GAA        96
105    Asp Gly Asp Gly Asn Arg Cys Asn Leu Leu His Arg Tyr Ser Leu Glu
106                    20                      25                      30
107    GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC TTC GCT GTT GTC ACA ACA       144
108    Glu Ile Leu Pro Tyr Leu Gly Trp Leu Val Phe Ala Val Val Thr Thr
109                    35                      40                      45
110    AGT TTT CTG GCG CTC CAG ATG TTC ATA GAC GCC CTT TAT GAG GAG CAG       192
111    Ser Phe Leu Ala Leu Gln Met Phe Ile Asp Ala Leu Tyr Glu Glu Gln
112            50                      55                      60
113    TAT GAA AGG GAT GTG GCC TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC       240
114    Tyr Glu Arg Asp Val Ala Trp Ile Ala Arg Gln Ser Lys Arg Met Ser
115    65                      70                      75                      80
116    TCT GTC GAT GAG GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC       288
117    Ser Val Asp Glu Asp Glu Asp Asp Glu Asp Asp Glu Asp Asp Tyr Tyr
118                            85                      90                      95
119    GAC GAC GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT       336
120    Asp Asp Glu Asp Asp Asp Asp Asp Ala Phe Tyr Asp Asp Glu Asp Asp
121                    100                     105                     110
122    GAG GAA GAA GAA TTG GAG AAC CTC ATG GAT GAT GAA TCA GAA GAT GAG       384
123    Glu Glu Glu Glu Leu Glu Asn Leu Met Asp Asp Glu Ser Glu Asp Glu
124                    115                     120                     125
125    GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA GCT GAG GAA ATG       432
126    Ala Glu Glu Glu Met Ser Val Glu Met Gly Ala Gly Ala Glu Glu Met
127            130                     135                     140
128    GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT GGC CAT CAT TTA AGG AAG       480
129    Gly Ala Gly Ala Asn Cys Ala Cys Val Pro Gly His His Leu Arg Lys
130    145                     150                     155                     160
131    AAT GAA GTG AAG TGT AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC       528
132    Asn Glu Val Lys Cys Arg Met Ile Tyr Phe Phe His Asp Pro Asn Phe
133                    165                     170                     175
134    CTG GTG TCT ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT       576
135    Leu Val Ser Ile Pro Val Asn Pro Lys Glu Gln Met Glu Cys Arg Cys
136                    180                     185                     190
137    GAA AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA GAG       624
138    Glu Asn Ala Asp Glu Glu Val Ala Met Glu Glu Glu Glu Glu Glu Glu
139                    195                     200                     210
140    GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT       672
141    Glu Glu Glu Glu Glu Glu Glu Met Gly Asn Pro Asp Gly Phe Ser Pro
142    220                     225                     230                     235
143
144    TAG                                                                  675
145
146
147
148    (2) INFORMATION FOR SEQ ID NO: 3:
149        (i) SEQUENCE CHARACTERISTICS:
150            (A) LENGTH:   228 base pairs
151            (B) TYPE:  nucleic acid
152            (C) STRANDEDNESS: single
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153              (D) TOPOLOGY:   linear
154         (ii) MOLECULE TYPE:  genomic DNA
155         (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 3:
156
157
158
159    GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG TTGTTTTTTT       60
160    TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA ATTTGATTTT GTTCTAAAGT      120
161    TCATTATGCA AAGATGTCAC CAACAGACTT CTGACTGCAT GGTGAACTTT CATATGATAC      180
162    ATAGGATTAC ACTTGTACCT GTTAAAAATA AAAGTTTGAC TTGCATAC                   228
163
164
165
166    (2) INFORMATION FOR SEQ ID NO: 4:
167         (i) SEQUENCE CHARACTERISTICS:
168              (A) LENGTH:  1365 base pairs
169              (B) TYPE:  nucleic acid
170              (C) STRANDEDNESS: single
171              (D) TOPOLOGY:  linear
172         (ii) MOLECULE TYPE:  genomic DNA
173         (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 4:
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175
176    ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT           50
177    GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT          100
178    CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG          150
179    AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT          200
180    CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA          250
181    CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT          300
182    AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCCTTT GCTCTCCCAG          350
183    CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG          400
184    CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT          450
185    ACCCTTTGTG CC                                                  462
186    ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA        504
187    GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG        546
188    TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC        588
189    TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC        630
190    ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC        672
191    TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG        714
192    GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC        756
193    GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT        798
194    GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA        840
195    GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA        882
196    GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT        924
197    GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT AGG ATG ATT        966
198    TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT ATA CCA GTG       1008
199    AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA AAT GCT GAT       1050
200    GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA GAG GAG GAG       1092
201    GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT       1134
202    TAG                                                          1137
203    GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG         1187
204    TTGTTTTTTT TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA         1237
205    ATTTGATTTT GTTCTAAAGT TCATTATGCA AAGATGTCAC CAACAGACTT         1287
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206    CTGACTGCAT GGTGAACTTT CATATGATAC ATAGGATTAC ACTTGTACCT      1337
207    GTTAAAAATA AAAGTTTGAC TTGCATAC                             1365
208
209
210                              -- --- -- --------- . -- -- -------
211    (2) INFORMATION FOR SEQ ID NO: 5:
212         (i) SEQUENCE CHARACTERISTICS:
213             (A) LENGTH:  4698 base pairs
214             (B) TYPE:  nucleic acid
215             (C) STRANDEDNESS: single
216             (D) TOPOLOGY:  linear
217         (ii) MOLECULE TYPE:  genomic DNA
218         (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 5:
219
220    ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT        50
221    GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT       100
222    CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG       150
223    AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT       200
224    CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA       250
225    CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT       300
226    AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCCTTT GCTCTCCCAG       350
227    CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG       400
228    CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT       450
229    ACCCTTTGTG CC                                               462
230    ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA      504
231    GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG      546
232    TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC      588
233    TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC      630
234    ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC      672
235    TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG      714
236    GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC      756
237    GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT      798
238    GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA      840
239    GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA      882
240    GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC T                916
241    GTGAGTAACC CGTGGTCTTT ACTCTAGATT CAGGTGGGGT GCATTCTTTA       966
242    CTCTTGCCCA CATCTGTAGT AAAGACCACA TTTTGGTTGG GGGTCATTGC      1016
243    TGGAGCCATT CCTGGCTCTC CTGTCCACGC CTATCCCCGC TCCTCCCATC      1066
244    CCCCACTCCT TGCTCCGCTC TCTTTCCTTT TCCCACCTTG CCTCTGGAGC      1116
245    TTCAGTCCAT CCTGCTCTGC TCCCTTTCCC CTTTGCTCTC CTTGCTCCCC      1166
246    TCCCCCTCGG CTCAACTTTT CGTGCCTTCT GCTCTCTGAT CCCCACCCTC      1216
247    TTCAGGCTTC CCCATTTGCT CCTCTCCCGA AACCCTCCCC TTCCTGTTCC      1266
248    CCTTTTCGCG CCTTTTCTTT CCTGCTCCCC TCCCCCTCCC TATTTACCTT      1316
249    TCACCAGCTT TGCTCTCCCT GCTCCCCTCC CCCTTTTGCA CCTTTTCTTT      1366
250    TCCTGCTCCC CTCCCCCTCC CCTCCCTGTT TACCCTTCAC CGCTTTTCCT      1416
251    CTACCTGCTT CCCTCCCCCT TGCTGCTCCC TCCCTATTTG CATTTTCGGG      1466
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255    TCACTCTGTA GACCAGGCTG GCCTCAAACT CAGAAATCTG CCTGCCTCTG      1666
256    CCTCCCAAAT GCTGGGATTA AAGGCTTGCA CCAGGACTGC CCCAGTGCAG      1716
257    GCCTTTCTTT TTTCTCCTCT CTGGTCTCCC TAATCCCTTT TCTGCATGTT      1766
258    AACTCCCCTT TTGGCACCTT TCCTTTACAG GACCCCCTCC CCCTCCCTGT      1816
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/819,669E*

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Line	Error	Original Text
31	Wrong Classification	(C) CLASSIFICATION: 435